RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/570,011

Source: IEWP

Date Processed by STIC: 3-8-06

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IFWP

RAW SEQUENCE LISTING   DATE: 03/08/2006
PATENT APPLICATION: US/10/570,011   TIME: 13:16:18

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03072006\J570011.raw**

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    3 <110> APPLICANT: Kureha Chemical Industry Company, Limited
    4        KAMATA, Toru
    5        MITSUSHITA, Junji
    7 <120> TITLE OF INVENTION: Antibodies to Nox1 polypeptide, method for the detection of
cancer using
    8        Nox1 gene and method for screening substances suppressing cancer growth
   10 <130> FILE REFERENCE: 0701012WO1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/570,011
C--> 12 <141> CURRENT FILING DATE: 2006-03-01
   12 <160> NUMBER OF SEQ ID NOS: 27
   14 <170> SOFTWARE: PatentIn version 3.1
   16 <210> SEQ ID NO: 1
   17 <211> LENGTH: 1734
   18 <212> TYPE: DNA
   19 <213> ORGANISM: Homo sapiens
   21 <220> FEATURE:
   22 <221> NAME/KEY: CDS
   23 <222> LOCATION: (71)..(1618)
   24 <223> OTHER INFORMATION: Human Nox1 polypeptide of SEQ NO:2
   27 <400> SEQUENCE: 1
   28 ggacctctcc agaatccgga ttgctgaatc ttccctgttg cctagaaggg ctccaaacca       60
   30 cctcttgaca atg gga aac tgg gtg gtt aac cac tgg ttt tca gtt ttg         109
   31             Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu
   32              1               5                      10
   34 ttt ctg gtt gtt tgg tta ggg ctg aat gtt ttc ctg ttt gtg gat gcc       157
   35 Phe Leu Val Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala
   36     15                  20                  25
   38 ttc ctg aaa tat gag aag gcc gac aaa tac tac tac aca aga aaa atc       205
   39 Phe Leu Lys Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile
   40 30                  35                  40                  45
   42 ctt ggg tca aca ttg gcc tgt gcc cga gcg tct gct ctc tgc ttg aat       253
   43 Leu Gly Ser Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn
   44                 50                  55                  60
   46 ttt aac agc acg ctg atc ctg ctt cct gtg tgt cgc aat ctg ctg tcc       301
   47 Phe Asn Ser Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser
   48                 65                  70                  75
   50 ttc ctg agg ggc acc tgc tca ttt tgc agc cgc aca ctg aga aag caa       349
   51 Phe Leu Arg Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln
   52         80                  85                  90
   54 ttg gat cac aac ctc acc ttc cac aag ctg gtg gcc tat atg atc tgc       397
   55 Leu Asp His Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys
   56     95                  100                 105
   58 cta cat aca gct att cac atc att gca cac ctg ttt aac ttt gac tgc       445
   59 Leu His Thr Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys
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60 110                    115                   120                   125
62 tat agc aga agc cga cag gcc aca gat ggc tcc ctt gcc tcc att ctc      493
63 Tyr Ser Arg Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu
64                    130                   135                   140
66 tcc agc cta tct cat gat gag aaa aag ggg ggt tct tgg cta aat ccc      541
67 Ser Ser Leu Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro
68                    145                   150                   155
70 atc cag tcc cga aac acg aca gtg gag tat gtg aca ttc acc agc att      589
71 Ile Gln Ser Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Ile
72          160                   165                   170
74 gct ggt ctc act gga gtg atc atg aca ata gcc ttg att ctc atg gta      637
75 Ala Gly Leu Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val
76      175                   180                   185
78 act tca gct act gag ttc atc cgg agg agt tat ttt gaa gtc ttc tgg      685
79 Thr Ser Ala Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp
80 190                   195                   200                   205
82 tat act cac cac ctt ttt atc ttc tat atc ctt ggc tta ggg att cac      733
83 Tyr Thr His His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His
84                    210                   215                   220
86 ggc att ggt gga att gtc cgg ggt caa aca gag gag agc atg aat gag      781
87 Gly Ile Gly Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu
88                    225                   230                   235
90 agt cat cct cgc aag tgt gca gag tct ttt gag atg tgg gat gat cgt      829
91 Ser His Pro Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg
92          240                   245                   250
94 gac tcc cac tgt agg cgc cct aag ttt gaa ggg cat ccc cct gag tct      877
95 Asp Ser His Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser
96      255                   260                   265
98 tgg aag tgg atc ctt gca ccg gtc att ctt tat atc tgt gaa agg atc      925
99 Trp Lys Trp Ile Leu Ala Pro Val Ile Leu Tyr Ile Cys Glu Arg Ile
100 270                   275                   280                   285
102 ctc cgg ttt tac cgc tcc cag cag aag gtt gtg att acc aag gtt gtt      973
103 Leu Arg Phe Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val
104                    290                   295                   300
106 atg cac cca tcc aaa gtt ttg gaa ttg cag atg aac aag cgt ggc ttc     1021
107 Met His Pro Ser Lys Val Leu Glu Leu Gln Met Asn Lys Arg Gly Phe
108                    305                   310                   315
110 agc atg gaa gtg ggg cag tat atc ttt gtt aat tgc ccc tca atc tct     1069
111 Ser Met Glu Val Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser
112          320                   325                   330
114 ctc ctg gaa tgg cat cct ttt act ttg acc tct gct cca gag gaa gat     1117
115 Leu Leu Glu Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp
116      335                   340                   345
118 ttc ttc tcc att cat atc cga gca gca ggg gac tgg aca gaa aat ctc     1165
119 Phe Phe Ser Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu
120 350                   355                   360                   365
122 ata agg gct ttc gaa caa caa tat tca cca att ccc agg att gaa gtg     1213
123 Ile Arg Ala Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val
124                    370                   375                   380
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Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\03072006\J570011.raw

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126 gat ggt ccc ttt ggc aca gcc agt gag gat gtt ttc cag tat gaa gtg     1261
127 Asp Gly Pro Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val
128         385             390             395
130 gct gtg ctg gtt gga gca gga att ggg gtc acc ccc ttt gct tct atc     1309
131 Ala Val Leu Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile
132         400             405             410
134 ttg aaa tcc atc tgg tac aaa ttc cag tgt gca gac cac aac ctc aaa     1357
135 Leu Lys Ser Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys
136     415             420             425
138 aca aaa aag gtt ggt cat gca gca tta aac ttt gac aag gcc act gac     1405
139 Thr Lys Lys Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp
140 430             435             440             445
142 atc gtg aca ggt ctg aaa cag aaa acc tcc ttt ggg aga cca atg tgg     1453
143 Ile Val Thr Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp
144         450             455             460
146 gac aat gag ttt tct aca ata gct acc tcc cac ccc aag tct gta gtg     1501
147 Asp Asn Glu Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val
148         465             470             475
150 gga gtt ttc tta tgt ggc cct cgg act ttg gca aag agc ctg cgc aaa     1549
151 Gly Val Phe Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys
152         480             485             490
154 tgc tgt cac cga tat tcc agt ctg gat cct aga aag gtt caa ttc tac     1597
155 Cys Cys His Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr
156     495             500             505
158 ttc aac aaa gaa aat ttt tga gttataggaa taaggacggt aatctgcatt        1648
159 Phe Asn Lys Glu Asn Phe
160 510             515
162 ttgtctcttt gtatcttcag taatttactt ggtctcgtca ggtttgagca gtcactttag   1708
164 gataagaatg tgcctctcaa gccttg                                        1734
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167 <210> SEQ ID NO: 2
168 <211> LENGTH: 515
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapiens
172 <400> SEQUENCE: 2

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174 Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu Phe Leu Val
175 1               5               10              15
178 Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys
179         20              25              30
182 Tyr Glu Lys Ala Asp Lys Tyr Tyr Thr Arg Lys Ile Leu Gly Ser
183         35              40              45
186 Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser
187     50              55              60
190 Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg
191 65              70              75              80
194 Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His
195             85              90              95
198 Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr
199         100             105             110
202 Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg
```

```
203          115                  120                  125
206 Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu
207      130                  135                  140
210 Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro Ile Gln Ser
211 145                  150                  155                  160
214 Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Ile Ala Gly Leu
215                  165                  170                  175
218 Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val Thr Ser Ala
219                  180                  185                  190
222 Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr His
223      195                  200                  205
226 His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His Gly Ile Gly
227      210                  215                  220
230 Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu Ser His Pro
231 225                  230                  235                  240
234 Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg Asp Ser His
235                  245                  250                  255
238 Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser Trp Lys Trp
239      260                  265                  270
242 Ile Leu Ala Pro Val Ile Leu Tyr Ile Cys Glu Arg Ile Leu Arg Phe
243      275                  280                  285
246 Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Met His Pro
247      290                  295                  300
250 Ser Lys Val Leu Glu Leu Gln Met Asn Lys Arg Gly Phe Ser Met Glu
251 305                  310                  315                  320
254 Val Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser Leu Leu Glu
255                  325                  330                  335
258 Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp Phe Phe Ser
259                  340                  345                  350
262 Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu Ile Arg Ala
263      355                  360                  365
266 Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val Asp Gly Pro
267      370                  375                  380
270 Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val Ala Val Leu
271 385                  390                  395                  400
274 Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile Leu Lys Ser
275                  405                  410                  415
278 Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys Thr Lys Lys
279      420                  425                  430
282 Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val Thr
283      435                  440                  445
286 Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn Glu
287      450                  455                  460
290 Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val Gly Val Phe
291 465                  470                  475                  480
294 Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys His
295                  485                  490                  495
298 Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr Phe Asn Lys
299                  500                  505                  510
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302 Glu Asn Phe
303         515
306 <210> SEQ ID NO: 3
307 <211> LENGTH: 2577
308 <212> TYPE: DNA
309 <213> ORGANISM: Rattus norvegicus
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (128)..(1819)
314 <223> OTHER INFORMATION: Rat Nox1 polypeptide of SEQ NO:4
317 <400> SEQUENCE: 3
318 ttctgagtag gtgtgcattt gagtgtcata aagacatata tcttgagcta gacagaagtt      60
320 cctatcctga aggatcccat cagagaaacc agattgctcc taagaggctc cagacctcca     120
322 tttgaca atg gga aac tgg ctg gtt aac cac tgg ctc tca gtt ttg ttt       169
323         Met Gly Asn Trp Leu Val Asn His Trp Leu Ser Val Leu Phe
324         1               5                   10
326 ctg gtt tct tgg ttg ggg ctg aac att ttt ctg ttt gtg tac gtc ttc       217
327 Leu Val Ser Trp Leu Gly Leu Asn Ile Phe Leu Phe Val Tyr Val Phe
328 15                  20                  25 .                30
330 ctg aat tat gag aag tct gac aag tac tat tac acg aga gaa att ctc       265
331 Leu Asn Tyr Glu Lys Ser Asp Lys Tyr Tyr Tyr Thr Arg Glu Ile Leu
332                 35                  40                  45
334 gga act gcc ttg gcc ttg gcc aga gca tct gct ttg tgc ctg aat ttt       313
335 Gly Thr Ala Leu Ala Leu Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe
336             50                  55                  60
338 aac agc atg gtg atc ctg att cct gtg tgt cga aat ctg ctc tcc ttc       361
339 Asn Ser Met Val Ile Leu Ile Pro Val Cys Arg Asn Leu Leu Ser Phe
340             65                  70                  75
342 ctg agg ggc acc tgc tca ttt tgc aac cac acg ctg aga aag cca ttg       409
343 Leu Arg Gly Thr Cys Ser Phe Cys Asn His Thr Leu Arg Lys Pro Leu
344         80                  85                  90
346 gat cac aac ctc acc ttc cat aag ctg gtg gca tat atg atc tgc ata       457
347 Asp His Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Ile
348 95                  100                 105                 110
350 ttc aca gct att cat atc att gca cat cta ttt aac ttt gaa cgc tac       505
351 Phe Thr Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Glu Arg Tyr
352                 115                 120                 125
354 agt aga agc caa cag gcc atg gat gga tct ctt gcc tct gtt ctc tcc       553
355 Ser Arg Ser Gln Gln Ala Met Asp Gly Ser Leu Ala Ser Val Leu Ser
356             130                 135                 140
358 agc cta ttc cat ccc gag aaa gaa gat tct tgg cta aat ccc atc cag       601
359 Ser Leu Phe His Pro Glu Lys Glu Asp Ser Trp Leu Asn Pro Ile Gln
360         145                 150                 155
362 tct cca aac gtg aca gtg atg tat gca gca ttt acc agt att gct ggc       649
363 Ser Pro Asn Val Thr Val Met Tyr Ala Ala Phe Thr Ser Ile Ala Gly
364         160                 165                 170
366 ctt act gga gtg gtc gcc act gtg gct ttg gtt ctc atg gta act tca       697
367 Leu Thr Gly Val Val Ala Thr Val Ala Leu Val Leu Met Val Thr Ser
368 175                 180                 185                 190
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/08/2006
PATENT APPLICATION: **US/10/570,011**   TIME: 13:16:19

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03072006\J570011.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

VERIFICATION SUMMARY   DATE: 03/08/2006
PATENT APPLICATION: **US/10/570,011**   TIME: 13:16:19

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\03072006\J570011.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date